I claim:

1. A method of mapping a polynucleotide, the method comprising the steps of:

(a) providing a plurality of populations of restriction fragments, the restriction fragments of each population having ends defined by digesting the polynucleotide with a plurality of combinations of restriction endonucleases;

(b) determining the nucleotide sequence of a portion of each end of each restriction fragment of each population so that a pair of nucleotide sequences is obtained for each restriction fragment of each population; and

(c) ordering the pairs of nucleotide sequences by matching the nucleotide sequences between pairs to form a map of the polynucleotide.

2. The method of claim 1 wherein said step of determining said nucleotide sequence of said end of each restriction fragment includes the steps of enzymatically removing a segment of nucleotides from each said end; ligating the segment of nucleotides from each said end together to form a pair of segments, ligating a sample of pairs of segments from said plurality of populations to form one or more concatenations of pairs of segments, and sequencing the concatenations of pairs of segments.

3. The method of claim 2 wherein said plurality of populations of restriction fragments is between 3 and 8, inclusive.

4. The method of claim 3 wherein said combinations of restriction endonucleases used for digesting said polynucleotide consist of three restriction endonucleases selected from a set of four restriction endonucleases.

5. The method of claim 3 wherein said combinations of restriction endonucleases used for digesting said polynucleotide consist of two restriction endonucleases selected from a set of three restriction endonucleases.

6. The method of claim 5 wherein said steps of enzymatically removing said segments of nucleotides is carried out with one of more type IIs restriction endonucleases.

7. The method of claim 6 wherein said segments of nucleotides consist of between 7 and 9 nucleotides.

8. A physical map of a polynucleotide comprising an ordered series of segments of nucleotides, the segments of nucleotides being adjacent to and including recognition sites in the polynucleotide of a plurality of predetermined restriction endonucleases.

9. The physical map of claim 8 wherein said ordered series comprises at least one hundred said segments of nucleotides and wherein said plurality of predetermined restriction endonucleases is between 2 and 6, inclusive.

10. The physical map of claim 9 wherein said segments of nucleotides of said ordered series are separated by unsequenced regions of said restriction fragments.

11. The physical map of claim 10 wherein said ordered series comprises at least one thousand said segments of nucleotides.

12. The physical map of claim 8 wherein said polynucleotide is between 180 kilobases and 1 megabase in length.

13. The physical map of claim 8 wherein said polynucleotide is a genome of a micro-organism.

14. A method of mapping a polynucleotide, the method comprising the steps of:

(a) providing a plurality of populations of restriction fragments, the restriction fragments of each population having an interior and ends defined by digesting the polynucleotide with a plurality of combinations of restriction endonucleases, and each restriction fragment being inserted into a vector;

(b) cleaving each vector to remove the interior of the restriction fragment and to leave a segment of each end of the restriction fragment in the vector;

(c) circularizing each vector so that the segments of each end of each restriction fragment are ligated together to form a pair of segments;

(d) determining the nucleotide sequences of a sample of pairs of segments to obtain a sample of pairs of nucleotide sequences; and

(e) ordering the pairs of nucleotide sequences by matching the nucleotide sequences between pairs to form a map of the polynucleotide.

15. The method of claim 14 wherein said step of determining said nucleotide sequences of said sample of said pairs of segments includes the steps of ligating said sample of pairs of segments from said plurality of populations to form one or more concatenations of pairs of segments, and sequencing the concatenations of pairs of segments.

16. The method of claim 15 wherein said sample includes a number of said pairs of segments large enough so that with a probability of ninety-nine percent every possible kind of pair of segments is represented in said sample.

17. The method of claim 16 wherein said step of cleaving is carried out with one or more type IIs restriction endonucleases.

18. A vector for cloning a fragment of DNA, the vector comprising: a first type IIs restriction site and a second type IIs restriction site such that a first type IIs restriction endonuclease recognizing the first type IIs restriction site has a cleavage site downstream from the first type IIs restriction site and such that a second type IIs restriction endonucleases recognizing the second type IIs restriction site has a cleavage site upstream from the second type IIs site.

19. The vector of claim 18 further including a third restriction site and a fourth restriction site for accepting said fragment of DNA, the third restriction site being immediately downstream of said first type IIs restriction site such that said cleavage site of said first type IIs restriction endonuclease is downstream of the third restriction site, and the fourth restriction site being immediately upstream of said second type IIs restriction site such that said cleavage site of said second type IIs restriction endonuclease is upstream of the fourth restriction site.

20. The vector of claim 19 further including a third type IIs restriction site and a fourth type IIs restriction site, the third type IIs restriction site being positioned upstream of said first type IIs restriction site such that a third type IIs restriction endonuclease recognizing the third type IIs restriction site has a cleavage site identical to that of said third restriction site, and the fourth type IIs restriction site being positioned downstream of said second type IIs restriction site such that a fourth type IIs restriction endonuclease recognizing the fourth type IIs restriction site has a cleavage site identical to that of said fourth restriction site.

21. A method of analyzing gene expression in a cell or tissue, the method comprising the steps of:

(a) forming a population of cDNA molecules from mRNA of a cell or tissue;

(b) determining the nucleotide sequence of a portion of each end of each cDNA molecule of the population so that a pair of nucleotide sequences is obtained for each cDNA of the population; and

(c) tabulating the pairs of nucleotide sequences to form a frequency distribution of gene expression in the cell or tissue.

22. The method of claim 21 wherein said step of determining said nucleotide sequence of said end of each restriction fragment includes the steps of enzymatically removing a segment of nucleotides from each said end; ligating the segment of nucleotides from each said end together to form a pair of segments, ligating a sample of pairs of segments from said population of cDNA molecules to form one or more concatenations of pairs of segments, and sequencing the concatenations of pairs of segments.